

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/922,449

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length.
Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/922,449

DATE: 10/02/2001
TIME: 16:21:47

Input Set: I922449.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

*see item 4
on Error
summary sheet*

1 <110> BioInside Gesellschaft fr Biodiagnostik, Auftragsforschung und Consulting
2 mbH
3 <120> Test kit and method for quantitatively detecting genetically modified DNA
4 in foodstuff by means of
5 fluorescence-coupled PCR
6 <130> PCT/EP00/
7 <140> US/09/922,449
8 <141> 2001-08-03
9 <150> DE 199 06 169,6
10 <151> 1999-02-08
11 <160> 25 OK, but see p. 3
12 <170> PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES FOLLOW

13 <210> 1
E--> 14 <211> 240
15 <212> DNA
16 <213> Artificial sequence
17 <220>
18 <223> Description of artificial sequence: Roundup soy gene (RRS gene)
19 <400> 1
20 gtcttcaaag caagtggatt gatgtgatat ctccactgac gtaagggatg acgcacaatc 60
E--> 21 ccactatcct tcgcaagacc cttcctctat ataaggaagt tcatttcatt tggagaggac
W--> 22 120
E--> 23 acgctgacaa gctgactcta gcagatcttt caagaatgac acaaattaac aacatggctc
W--> 24 180
E--> 25 aagggaatac aacccttaac cccaattcca attccataa accccaagtt cctaaatctt
W--> 26 240
see item 1 on Error summary sheet
120
180
240

27 <210> 8
E--> 28 <211> 142
29 <212> DNA
30 <213> Artificial sequence
31 <220>
32 <223> Description of artificial sequence: target IAC DNA for the RRS gene
33 <400> 8
E--> 34 catttggaga ggacacgctg aggacgttcg ccaattttcg cctcccacgt ctcaccgagc 60
W--> 35
E--> 36 cgaaggtttt acgttttccc
W--> 37
E--> 38 tcgttttcat ccagtctttc 120
see p. 4

PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/09/922,449

DATE: 10/02/2001
TIME: 16:21:47

Input Set: I922449.RAW

39 atggctcaag ggatacaaac cc 142

E--> 40 <210> 8a
E--> 41 <211> 143
42 <212> DNA
43 <213> Artificial sequence
44 <220>
45 <223> Description of artificial sequence: target IAC DNA for the RRS gene
46 <400> 8a
E--> 47 ctgacgtaag ggatgacgca cggacgttcg ccaattttcg cctccccacgt ctcaccgagc 60
W--> 48
E--> 49 cgaagggtttt acgttttccc
W--> 50
E--> 51 tcgttttcat ccagtctttg 120
52 acaagctgac tctagcagat ctt 143

see pp 3 & 4 (same error)

53 <210> 10
E--> 54 <211> 150
55 <212> DNA
56 <213> Artificial sequence
57 <220>
58 <223> Description of artificial sequence: reference IAC DNA for the RRS gene
59 <400> 10
E--> 60 gccctctact ccacccccat ccggacgttc gccaattttc gcctccccacg tctcaccgag 60
W--> 61
E--> 62 acgaagggttt tacgttttcc
W--> 63
E--> 64 ttcgttttca tccagtcttt 120
65 gacaatcggc ttgcagatgg gcttgcccttc 150

see pp 3 & 4

66 <210> 11
E--> 67 <211> 250
68 <212> DNA
69 <213> Artificial sequence
70 <220>
71 <223> Description of artificial sequence: lectin gene
72 <400> 11
E--> 73 gggaaggtta caactcaata aggttgacga aaacggcacc ccaaaaccct cgtctcttgg 60
W--> 74
E--> 75 tactccaccc ccattccacat
W--> 76
E--> 77 gaaaccggta gcgttgccag 120 cttcgccgct tccttcaact tcaccttcta tgccccagac
W--> 78
E--> 79 ttgcagatgg 180 gcttgcccttc
W--> 80
E--> 81 caattgacac taagccacaa acacatgcag gttatcttgg 240
82 tcttttcaac 250

pp 3 & 4

This needs to be
changed to 3

09/92 449 3

<210> 2a
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of artificial sequence: probe
<400> 2a 3
cccactatcc ttcgcaagac ctt

invalid - Per 1.821 of Sequence Rules,

"Each sequence
set forth in the
'Sequence Listings' shall
be

assigned
a separate
sequence
identifier.

The sequence
identifiers shall
begin with 1
and increase
sequentially by
integers."

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

009224494

<210> 8
<211> 142
<212> DNA
<213> Artificial sequence

<220>

<223> Description of artificial sequence: target IAC DNA for the RRS gene

<400> 8

catttggaga ggacacgctg aggacgttcg ccaattttcg cctcccacgt ctcaccgagc 60 gtggtgttta

cgaagggtttt acgttttccc gtatcccctt

~~tcgttttcat ccagtctttc 120~~

atggctcaag ggatacaaac cc

142

insert a
hard
return

These format errors exist
throughout submitted file.

Input Set: I922449.RAW

| Line | Error/Warning | Original Text |
|------|---|---|
| 14 | E Input 240, Calc# Bases 60 differ | <211> 240 |
| 21 | E Wrong Amino Acid Designator | ccactatcct tcgcaagacc cttcctctat ataaggaa |
| 21 | E Wrong Amino Acid Designator | ccactatcct tcgcaagacc cttcctctat ataaggaa |
| 21 | E Wrong Amino Acid Designator | ccactatcct tcgcaagacc cttcctctat ataaggaa |
| 21 | E Wrong Amino Acid Designator | ccactatcct tcgcaagacc cttcctctat ataaggaa |
| 21 | E Wrong Amino Acid Designator | ccactatcct tcgcaagacc cttcctctat ataaggaa |
| 21 | E Wrong Amino Acid Designator | ccactatcct tcgcaagacc cttcctctat ataaggaa |
| 22 | W Invalid/Missing Amino Acid Numbering | 120 |
| 23 | E Wrong Amino Acid Designator | acgctgacaa gctgactcta gcagatcttt caagaatg |
| 23 | E Wrong Amino Acid Designator | acgctgacaa gctgactcta gcagatcttt caagaatg |
| 23 | E Wrong Amino Acid Designator | acgctgacaa gctgactcta gcagatcttt caagaatg |
| 23 | E Wrong Amino Acid Designator | acgctgacaa gctgactcta gcagatcttt caagaatg |
| 23 | E Wrong Amino Acid Designator | acgctgacaa gctgactcta gcagatcttt caagaatg |
| 23 | E Wrong Amino Acid Designator | acgctgacaa gctgactcta gcagatcttt caagaatg |
| 24 | W Invalid/Missing Amino Acid Numbering | 180 |
| 25 | E Wrong Amino Acid Designator | aaggataca aacccttaat cccaattcca atttccat |
| 25 | E Wrong Amino Acid Designator | aaggataca aacccttaat cccaattcca atttccat |
| 25 | E Wrong Amino Acid Designator | aaggataca aacccttaat cccaattcca atttccat |
| 25 | E Wrong Amino Acid Designator | aaggataca aacccttaat cccaattcca atttccat |
| 25 | E Wrong Amino Acid Designator | aaggataca aacccttaat cccaattcca atttccat |
| 25 | E Wrong Amino Acid Designator | aaggataca aacccttaat cccaattcca atttccat |
| 26 | W Invalid/Missing Amino Acid Numbering | 240 |
| 28 | E Input 142, Calc# Bases 42 differ | <211> 142 |
| 34 | E Wrong Amino Acid Designator | catttgagga ggacacgctg aggacgttcg ccaatttt |
| 34 | E Wrong Amino Acid Designator | catttgagga ggacacgctg aggacgttcg ccaatttt |
| 34 | E Wrong Amino Acid Designator | catttgagga ggacacgctg aggacgttcg ccaatttt |
| 34 | E Wrong Amino Acid Designator | catttgagga ggacacgctg aggacgttcg ccaatttt |
| 34 | E Wrong Amino Acid Designator | catttgagga ggacacgctg aggacgttcg ccaatttt |
| 34 | E Wrong Amino Acid Designator | catttgagga ggacacgctg aggacgttcg ccaatttt |
| 35 | W Invalid/Missing Amino Acid Numbering | |
| 36 | E Wrong Amino Acid Designator | cgaagggtttt acgtttttccc gtatccccctt |
| 36 | E Wrong Amino Acid Designator | cgaagggtttt acgtttttccc gtatccccctt |
| 36 | E Wrong Amino Acid Designator | cgaagggtttt acgtttttccc gtatccccctt |
| 37 | W Invalid/Missing Amino Acid Numbering | |
| 38 | E Number of Bases conflict w/ Running Total | tcgttttcat ccagtctttc 120 |
| 40 | E Wrong Sequence Number 8 | <210> 8a |
| 41 | E Input 143, Calc# Bases 43 differ | <211> 143 |
| 47 | E Wrong Amino Acid Designator | ctgacgtaag ggatgacgca cggacgttcg ccaatttt |
| 47 | E Wrong Amino Acid Designator | ctgacgtaag ggatgacgca cggacgttcg ccaatttt |
| 47 | E Wrong Amino Acid Designator | ctgacgtaag ggatgacgca cggacgttcg ccaatttt |
| 47 | E Wrong Amino Acid Designator | ctgacgtaag ggatgacgca cggacgttcg ccaatttt |
| 47 | E Wrong Amino Acid Designator | ctgacgtaag ggatgacgca cggacgttcg ccaatttt |
| 47 | E Wrong Amino Acid Designator | ctgacgtaag ggatgacgca cggacgttcg ccaatttt |
| 48 | W Invalid/Missing Amino Acid Numbering | |
| 49 | E Wrong Amino Acid Designator | cgaagggtttt acgtttttccc gtatccccctt |
| 49 | E Wrong Amino Acid Designator | cgaagggtttt acgtttttccc gtatccccctt |
| 49 | E Wrong Amino Acid Designator | cgaagggtttt acgtttttccc gtatccccctt |
| 50 | W Invalid/Missing Amino Acid Numbering | |

Input Set: I922449.RAW

Line ? Error/Warning

Original Text

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51 E Number of Bases conflict w/ Running Total tcgttttcat ccagtctttg 120
54 E Input 150, Calc# Bases 50 differ <211> 150
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
60 E Wrong Amino Acid Designator gccctctact ccacccccat ccggacgttc gccaatth
61 W Invalid/Missing Amino Acid Numbering
62 E Wrong Amino Acid Designator acgaagggtt tacgttttcc cgtatcccct
62 E Wrong Amino Acid Designator acgaagggtt tacgttttcc cgtatcccct
62 E Wrong Amino Acid Designator acgaagggtt tacgttttcc cgtatcccct
63 W Invalid/Missing Amino Acid Numbering
64 E Number of Bases conflict w/ Running Total ttcgttttca tccagtcttt 120
67 E Input 250, Calc# Bases 50 differ <211> 250
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
73 E Wrong Amino Acid Designator gggaaagtta caactcaata aggttgacga aaacggca
74 W Invalid/Missing Amino Acid Numbering
75 E Wrong Amino Acid Designator tactccaccc ccattccacat ttgggacaaa
75 E Wrong Amino Acid Designator tactccaccc ccattccacat ttgggacaaa
75 E Wrong Amino Acid Designator tactccaccc ccattccacat ttgggacaaa
76 W Invalid/Missing Amino Acid Numbering
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
77 E Wrong Amino Acid Designator gaaaccggta gcgttgccag 120 cttcgccgct tcct
78 W Invalid/Missing Amino Acid Numbering
79 E Wrong Amino Acid Designator ttgcagatgg 180 gcttgccctt tttctcgac
79 E Wrong Amino Acid Designator ttgcagatgg 180 gcttgccctt tttctcgac
79 E Wrong Amino Acid Designator ttgcagatgg 180 gcttgccctt tttctcgac
80 W Invalid/Missing Amino Acid Numbering
81 E Number of Bases conflict w/ Running Total caattgacac taagccacaa acacatgcag gttatctt

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